1631

OIPE

P.S #4

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```
                  RAW SEQUENCE LISTING            DATE: 06/07/2000
                  PATENT APPLICATION:  US/09/521,640   TIME: 11:22:31

                  Input Set : D:\BACENDTAB_FINAL_RETREATS.rpt
                  Output Set: N:\CRF3\06072000\I521640.raw

        1 <110> APPLICANT: Byrum, Joseph R.
        2        Halling, Conrad H.
        3        Kovalic, David K.
        5 <120> TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
        6        Plants
        8 <130> FILE REFERENCE: 38-21(15750)D
C-->   10 <140> CURRENT APPLICATION NUMBER: US/09/521,640
C-->   10 <141> CURRENT FILING DATE: 2000-03-10
       10 <160> NUMBER OF SEQ ID NOS: 304701
       12 <210> SEQ ID NO: 1
       13 <211> LENGTH: 619
       14 <212> TYPE: DNA
       15 <213> ORGANISM: Glycine max
       17 <223> OTHER INFORMATION: unsure at all n locations
W-->   18 <400> SEQUENCE: 1
W-->   20 tggggaatat gcctgangta cactatagat actaagctag cngccagtgt agcctatcct   60
W-->   22 aatttgaccg ctggaacata cattggcttt ttagcntgaa tcgcctattg catgaacaac  120
W-->   24 attcaaaaca actaaatngc cttgggctta gcgagactga ctcgcttanc ccatgcttat  180
       26 tcaaactata taggcatggt gtcttagcag gactgactct cttatccacc aacagaatac  240
W-->   28 cacaagcctc atagactccg acctaagcaa actaactcgc ttatcacggc atgtcngcta  300
W-->   30 tcaagttcat actaactcag aagatataac tagagatnta tactcttngc tagccgaagt  360
W-->   32 gcaggggctt aacgagttcg tcataaaagc atagatttaa catanatgat gaacatgctt  420
W-->   34 agcgggacaa gaccgactta ctgatgtcat catataaccc anaatatcat ccanaataat  480
W-->   36 agactggcta ntgagcagct cgctagcaga catcaaagtt cagaaatatg nggctcaaga  540
       38 cccacatcta gtactatatg ctatactata gtcaaacatg aatgacctca tatcctgaat  600
       40 aatccctaca ctatagtag                                                 619
       43 <210> SEQ ID NO: 2
       44 <211> LENGTH: 465
       45 <212> TYPE: DNA
       46 <213> ORGANISM: Glycine max
       48 <223> OTHER INFORMATION: unsure at all n locations
W-->   49 <400> SEQUENCE: 2
       51 ggggagtatc gtgagttcac tcaatattag cccttcagac tcgctgtaag acctcggtcc   60
       53 agccgaatcc ctttatgagc gcttaagtca ctgccgcgct tacacgcgga ctgagaaacc  120
       55 tgcgtacccg ctaatctctt cacacatccc ctatcgcact ggcggtatct caatgaccac  180
       57 catcgccttc caaccatgcc aactaatggc aatggccctg atcggatttc tcttaccatt  240
       59 gtcggattta cccgctatgg cgcttcatca acagaggatg ccctagtatc accctaccca  300
       61 caccccgtga ccaaccttgg cctttaaata aaacctatct ttgtcatttc ggaataaact  360
W-->   63 ttcctgtctt tcagcaaatg aagaacccct gctcntcct ttgggcgggc cttttgcacg  420
W-->   65 cttttggac ttgttatcaa aaaaaccctt cttgttcaaa acacn             465
       68 <210> SEQ ID NO: 3
       69 <211> LENGTH: 175
       70 <212> TYPE: DNA
       71 <213> ORGANISM: Glycine max
       73 <400> SEQUENCE: 3
       75 ggacttagta cgcgcttact gttacatata ctacctatgg caaatttgtt ttacactgaa   60
       77 ttacaacctt gtatgcacaa cgtatggtac tccttttgt tgcagttagt gaccattggg  120
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        79 gagtatgaac aggcatgaaa acacttaaag tcactttgga ataacacgac aaggt        175
        82 <210> SEQ ID NO: 4
        83 <211> LENGTH: 247
        84 <212> TYPE: DNA
        85 <213> ORGANISM: Glycine max
        87 <223> OTHER INFORMATION: unsure at all n locations
W--> 88 <400> SEQUENCE: 4
W--> 90 tctatacctg ttgcaagagn ttgtggtcta cgttcttctg cagatcacca tacagatctc    60
        92 tgtccttctt tgtagcaatc tggagtcaat gagaaacctg aagcttatgc tgtaaacatt   120
W--> 94 tataatagac ctcctcagca acanaactaa caacagcaga ataattatga cctttcaagc   180
W--> 96 aatagatgca atctaggttg gaggaatcat ccaaatctga gatggacaag tnctccgcaa   240
        98 caacaac                                                             247
       101 <210> SEQ ID NO: 5
       102 <211> LENGTH: 337
       103 <212> TYPE: DNA
       104 <213> ORGANISM: Glycine max
       106 <223> OTHER INFORMATION: unsure at all n locations
W--> 107 <400> SEQUENCE: 5
       109 gagtcctctc acgaggtgga ggttgagcca tgttctcagt ataaaaatta gtagtggaat    60
W--> 111 gctcanaatc agaatattca aaatcaccct caagagaatg ctcacaatgc acataatgac   120
       113 caggatgcac agtatgccta attaatctat gaaaggatct atctatttca agatcaaagg   180
       115 gttgtaaatc acctagaatg cccctagtca tgcactatat ccagcaaata atgtgtttct   240
W--> 117 taacaagcac ctaaccaggn ggtaaaacta caactatact caaacgatat caaaatgagc   300
W--> 119 cttaaatttg tgaggaacac cctanaatca tgaaaag                              337
       122 <210> SEQ ID NO: 6
       123 <211> LENGTH: 211
       124 <212> TYPE: DNA
       125 <213> ORGANISM: Glycine max
       127 <223> OTHER INFORMATION: unsure at all n locations
W--> 128 <400> SEQUENCE: 6
W--> 130 gagatgatgc gctccatgag tatgtggatc anatggagaa tagagatcat aatgaagaag    60
       132 aaaggaggag aagagggaat gatggtgttc ctagacaaaa ccgaattgat ggtattaaac   120
       134 tcaacattcc tccatttaaa ggaaagaatg atccggaggc ctacgtggag tgggagatga   180
       136 aaatagagca tgttttctca tgcaacaact a                                  211
       139 <210> SEQ ID NO: 7
       140 <211> LENGTH: 482
       141 <212> TYPE: DNA
       142 <213> ORGANISM: Glycine max
       144 <223> OTHER INFORMATION: unsure at all n locations
W--> 145 <400> SEQUENCE: 7
W--> 147 agcctgtgtc ctgaanattt gaanntcatt cacctgaggt ggcnacctct gaacttctac    60
       149 agaatgagct ctgatccact ggtatacaag ggcctcagat atcttaagaa cggggggttg   120
       151 attaagatat taccaactat ttcccccagt aaaaatctat ttcactttct atttcaggta   180
       153 ccaaatccct taaccatgga ctcttaaata atgattccaa ttgaaccatt ttgatgttaa   240
W--> 155 tataaaacca ttattaatta aagaagttca cggaagagaa agtgcanacc tggatttata   300
       157 ctgggtcggt acaccttgtg ctacgtccgt cccagaaccg ctgaagtcat attgaaatct   360
       159 tcagttgaca cagcatctct ggtaatttca caaacctgtt atcttgataa aaagaatact   420
       161 ttgaaatatt cttgcccagt ctagatgagg tgcagattaa gaaagttgtt aaaacctggt   480
       163 aa                                                                  482
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RAW SEQUENCE LISTING   DATE: 06/07/2000
PATENT APPLICATION: US/09/521,640   TIME: 11:22:31

Input Set : D:\BACENDTAB_FINAL_RETREATS.rpt
Output Set: N:\CRF3\06072000\I521640.raw

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      166 <210> SEQ ID NO: 8
      167 <211> LENGTH: 574
      168 <212> TYPE: DNA
      169 <213> ORGANISM: Glycine max
      171 <223> OTHER INFORMATION: unsure at all n locations
W--> 172 <400> SEQUENCE: 8
W--> 174 ntatcacttg aggacctatg atactaagct ctataaagtt acttgtcgaa ccaatcaaat    60
W--> 176 aagttttcaa ctagtaaaaa atgttagaaa tttatgtgaa atttntacca aagatagtca   120
W--> 178 ttgtatagtt gcttatttca agccatacaa aaatntaatt tgcatacttt attgtcatga   180
W--> 180 ttagaaagaa canaaccatg tgttgttcca agcataaaan aataagacca aaactttcac   240
W--> 182 cagtcgtgct ctnttttttc ttgagggtta tatatatata tatatatata tatatatata   300
W--> 184 tatatatata tatatatata tatatatata tanagaatca taacatgttt tgataggtac   360
      186 atgataagaa atggatcatt cagtaataaa cattttaaa tatactatac aatgcttaca    420
W--> 188 tcctagagat acatatatta taccatcatg cacnaaacct gagagaaatt tagtactata   480
W--> 190 tcacgagaaa gacacatgcc tttctgtttg tcctattatc attataanan aaacttggna   540
      192 ttaaacatac agcacaattc tttgtttatc gtaa                              574
      195 <210> SEQ ID NO: 9
      196 <211> LENGTH: 622
      197 <212> TYPE: DNA
      198 <213> ORGANISM: Glycine max
      200 <223> OTHER INFORMATION: unsure at all n locations
W--> 201 <400> SEQUENCE: 9
W--> 203 tggggatata tgccttgang ttcactnncn atgnctangn ccactatcga gtactcaagc    60
W--> 205 ttgtanatat tactcntata cattgcctgt tccattatgc tcttgatgtc cttatatgtt   120
      207 acttcgctcg tgacatcttt tgtcttgaat cggaatgaca tgacacggtt atctgtactg   180
W--> 209 tctntnngta ttggtagttg atatcgcgtt gcgggaggta attccgattg gattaactca   240
W--> 211 ccatccttaa cttgccanna ttgtatgaca tttgttgttg gatcacctat gatgtcttgt   300
W--> 213 ttccaacggt aatctatatc atttctgatg gcataagcat gaaaccaatc aaagaanagg   360
W--> 215 acattaatct tgactctttc acanantcgt agaactngct tggatttgtn tctgtttgac   420
W--> 217 cctttgtaaa gtggaaaacc atctctttat ggtcattctc cngagaataa aatctttcta   480
W--> 219 anggttnctt atcanntgct aagtgcagat acatcataag gtncataaaa aagtatgtgg   540
W--> 221 gattgatcga ctttggcgnc tcttgtcttg gtgatgtgtc taggatctna aagangctat   600
      223 tcttgagtta cagaagactg tg                                          622
      226 <210> SEQ ID NO: 10
      227 <211> LENGTH: 250
      228 <212> TYPE: DNA
      229 <213> ORGANISM: Glycine max
      231 <223> OTHER INFORMATION: unsure at all n locations
W--> 232 <400> SEQUENCE: 10
W--> 234 ccttcacccg acgaagacac tgacananac ttatcttctc cttcttggac aaagtatggc    60
W--> 236 aggctgnggg gcaagtaaat ttcttcccat cagaccttgg atgcaactat gatcgtatac   120
W--> 238 ccatatcagc tacatcttga cnggtattca agccatcctt tgtcttgcct ttgaatgtaa   180
W--> 240 ggaacgtccc aatgacacta tcacagacat tnttctccac atgcataaca tcaatacaat   240
      242 gtctaacgtc                                                        250
      245 <210> SEQ ID NO: 11
      246 <211> LENGTH: 536
      247 <212> TYPE: DNA
      248 <213> ORGANISM: Glycine max
      250 <223> OTHER INFORMATION: unsure at all n locations
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RAW SEQUENCE LISTING   DATE: 06/07/2000
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Input Set : D:\BACENDTAB_FINAL_RETREATS.rpt
Output Set: N:\CRF3\06072000\I521640.raw

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W--> 251 <400> SEQUENCE: 11
W--> 253 tgatgncntt nnnaattgac gcacgtanta ggtacactat aatactcagc gttcgagaaa    60
W--> 255 ccacttaaac taaggaagtt cctanacaaa aatcaatgga ggaagcttcg ccaagtatgc   120
W--> 257 gcattgaaga caccttattc aaacctttca aagttagtga gaaggctgaa cgaancacta   180
     259 gggaacttag aacaactaaa tccttaatgg aatgcgtagg tgacaatcat agtgaattac   240
     261 taaacaagat tggtagttac taatggcatt cagatactcc caagcctcga taatacttct   300
W--> 263 aaatggtata agaagacctn cacataataa tgtattaatg aagatgtgac cngactagat   360
     265 aaccactgag atgaatagtg cagaaagata taatccataa ttcaacctga aacacctcaa   420
     267 tattatcacg tcgctgcgtg actctttaga gaagagtaaa caattagagt tagtgaacac   480
W--> 269 tcatgatgac taatgcaacg attactctga tcctcactat actgtgccat acaacn       536
     272 <210> SEQ ID NO: 12
     273 <211> LENGTH: 210
     274 <212> TYPE: DNA
     275 <213> ORGANISM: Glycine max
     277 <400> SEQUENCE: 12
     279 tcatcttgct tggacgatga gaaaactggt gcaaatgaag agggtgagaa ggatggagaa    60
     281 acccatgctg tgactgtcat tcctatacgg ccaagttccc caccagctca acaccatcat   120
     283 tactcagcca atatcagtca ttctcattac ccaccaccca tttatccata aaggctatcc   180
     285 ctaaatcaac aacaaaaccc acctaccaca                                    210
     288 <210> SEQ ID NO: 13
     289 <211> LENGTH: 397
     290 <212> TYPE: DNA
     291 <213> ORGANISM: Glycine max
     293 <223> OTHER INFORMATION: unsure at all n locations
W--> 294 <400> SEQUENCE: 13
W--> 296 ttgatcatcc tgctntgata aataagaaag cctgggaaaa tggagacaat aagaaggagg    60
     298 gaggaaccca tgctgtgatt gccgttccta cttggccaaa tttcccacca gctcaacaat   120
     300 gtcaatactc aaccaatatc agcccttctc attacccacc accctattag tcaagaacac   180
W--> 302 ccaatcatcc acaaaggcca cccctgaatc agccacanag cttgcttgcc gcacatncga   240
W--> 304 tactaaacac caccactaac acanatcana acaccaacca gggaanggaa tttcagaaaa   300
     306 taagcctgca gaatcaccca attctggtgc atatgctaac tacttcatat tactcataat   360
W--> 308 caatggcaca taccccacca nggtctcaac tcatttt                            397
     311 <210> SEQ ID NO: 14
     312 <211> LENGTH: 548
     313 <212> TYPE: DNA
     314 <213> ORGANISM: Glycine max
     316 <223> OTHER INFORMATION: unsure at all n locations
W--> 317 <400> SEQUENCE: 14
W--> 319 ngatgtgagg aagtgtggaa gagtcagtct tcctactntt gtttgttgac catatattgg    60
W--> 321 tacctggaga tatgtcgcan gggtcacgag acctctgtga ggtcaggtgg agtgctatnt   120
W--> 323 cccaaaacca agcttgacca atcccaaccc aacctgngca tattcagtca gtgtgaacct   180
W--> 325 gtgacgtacc taagcaggcg agcttctgac agtcaaccca tattagaaca aagaccacac   240
     327 agcaaggagg ctcgtgtggc agctggccag ctatggatct tgagtggtat ctggagatag   300
     329 gcctctcgta atcgattacc cagggtgtgt aatcgattac atgggctaca aatggagacc   360
     331 agaagttaag atggcctctg ggtatcgatt accaacgggt gtgtaatcga ttaccatgct   420
W--> 333 tannaatgga nacagngagt taagatggcc tctggtatcc attaccaacg ggtgtaacga   480
W--> 335 tacanagcta aacatgagac ggatgtgcgn ggctctgtat ccataaccat gatttattca   540
W--> 337 ataccaan                                                           548
     340 <210> SEQ ID NO: 15
```

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RAW SEQUENCE LISTING              DATE: 06/07/2000
PATENT APPLICATION:  US/09/521,640   TIME: 11:22:31

Input Set :  D:\BACENDTAB_FINAL_RETREATS.rpt
Output Set:  N:\CRF3\06072000\I521640.raw
```

```
        341 <211> LENGTH: 598
        342 <212> TYPE: DNA
        343 <213> ORGANISM: Glycine max
        345 <223> OTHER INFORMATION: unsure at all n locations
W--> 346 <400> SEQUENCE: 15
W--> 348 tatatgtact tgacncgtcg atctctgagt cacctgcggc atgcaagctt anaaatatat   60
W--> 350 ggngattatg tnntggtatg tatgaattac atcacagata atttgattga ctaagattaa  120
        352 gtgatgatgg tggtggtaga tctgatgacc atcacagtga agaccacagt gatggtggtt  180
        354 gcaagcatgg agctgaagag gaacatgaaa ctaatatatg tgatttgaca gggagcacac  240
        356 aaaggttctg cattgcggca gtgaagaaca tgcttttgat ttctatacta gatatgccag  300
        358 atgtcatggg ttggatgtga gaaaatatga catacttcga gaatttgaat ggggaatgta  360
W--> 360 taaaacattg gttttcttgc atagaanagg gttgagaaaa aagaacactt cacgagggtc  420
        362 gatagaataa gagacatata tattcatact aattgtgagc taggctcatg tttcttagat  480
        364 agaaacataa catgaaagtc tttattcaca gaatataaca tgactaccca ccactgtatt  540
W--> 366 atatatccaa gatcgggata ctatttgata actagcngat agtgataatt gtgtgacn     598
        369 <210> SEQ ID NO: 16
        370 <211> LENGTH: 226
        371 <212> TYPE: DNA
        372 <213> ORGANISM: Glycine max
        374 <223> OTHER INFORMATION: unsure at all n locations
W--> 375 <400> SEQUENCE: 16
W--> 377 gtgtacacat gttgtaactt tcttgaatga aagtcttatg agatacaatt canagttcca   60
W--> 379 cttctctccc tctnttattc cttcaatntc gtgctcccgc cttctctctn tcttttcctc  120
        381 cattaaagta tcctcttcaa gcttcttatc caagggcaat tgtggtggtg aagctccttc  180
        383 ttccttggct gattccctag tggatggtgc cacccctctc ctcttc                 226
        386 <210> SEQ ID NO: 17
        387 <211> LENGTH: 193
        388 <212> TYPE: DNA
        389 <213> ORGANISM: Glycine max
        391 <223> OTHER INFORMATION: unsure at all n locations
W--> 392 <400> SEQUENCE: 17
W--> 394 atgacattnt aattctgcaa ataacaataa ctaaaccctt tatgtactag attagagact   60
W--> 396 aaagaaaggg attnttcttt tcctttttct cattcgtggc tttatcccct gacatttact  120
W--> 398 agacttgtgc ttccacatca tatatcccta tcattctgtc tttaatcatt canaaattca  180
        400 tttgatcttg tct                                                     193
        403 <210> SEQ ID NO: 18
        404 <211> LENGTH: 157
        405 <212> TYPE: DNA
        406 <213> ORGANISM: Glycine max
        408 <223> OTHER INFORMATION: unsure at all n locations
W--> 409 <400> SEQUENCE: 18
        411 ttaagttaaa aagtcttttt tcaacaaatt actctctggt aatcgattac cagaggatgt   60
W--> 413 aatcgattac cagtggccaa aactgantta caacagctat taaaatntga attcaaaatt  120
        415 tgcactgtgt aatcgattac acatatatgg taatcga                           157
        418 <210> SEQ ID NO: 19
        419 <211> LENGTH: 406
        420 <212> TYPE: DNA
        421 <213> ORGANISM: Glycine max
        423 <400> SEQUENCE: 19
```

Please Note:
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.**

VERIFICATION SUMMARY   DATE: 06/07/2000
PATENT APPLICATION: US/09/521,640   TIME: 11:22:32

Input Set : D:\BACENDTAB_FINAL_RETREATS.rpt
Output Set: N:\CRF3\06072000\I521640.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:18 M:283 W: Missing Blank Line separator, <400> field identifier
L:20 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:20 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:20 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:20 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:22 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:22 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:22 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:24 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:24 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:24 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:28 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:28 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:28 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:30 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:30 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:30 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:32 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:32 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:32 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:34 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:34 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:34 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:36 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:36 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:36 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:49 M:283 W: Missing Blank Line separator, <400> field identifier
L:63 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:63 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:63 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:63 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:65 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:65 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:65 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
M:340 Repeated in SeqNo=2
L:88 M:283 W: Missing Blank Line separator, <400> field identifier
L:90 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:90 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:90 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:90 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
L:94 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:94 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:94 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
M:340 Repeated in SeqNo=4
L:96 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4

VERIFICATION SUMMARY   DATE: 06/07/2000
PATENT APPLICATION: US/09/521,640   TIME: 11:22:32

Input Set : D:\BACENDTAB_FINAL_RETREATS.rpt
Output Set: N:\CRF3\06072000\I521640.raw

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L:96 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:96 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:107 M:283 W: Missing Blank Line separator, <400> field identifier
L:111 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:111 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:111 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:111 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:117 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:117 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:117 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
M:340 Repeated in SeqNo=5
L:119 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:119 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:119 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:128 M:283 W: Missing Blank Line separator, <400> field identifier
L:130 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:130 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:130 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:145 M:283 W: Missing Blank Line separator, <400> field identifier
L:147 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
M:340 Repeated in SeqNo=7
L:172 M:283 W: Missing Blank Line separator, <400> field identifier
L:174 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
M:340 Repeated in SeqNo=8
L:201 M:283 W: Missing Blank Line separator, <400> field identifier
L:203 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
M:340 Repeated in SeqNo=9
L:232 M:283 W: Missing Blank Line separator, <400> field identifier
L:234 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
M:340 Repeated in SeqNo=10
L:251 M:283 W: Missing Blank Line separator, <400> field identifier
L:253 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
M:340 Repeated in SeqNo=11
L:294 M:283 W: Missing Blank Line separator, <400> field identifier
L:296 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
M:340 Repeated in SeqNo=13
L:317 M:283 W: Missing Blank Line separator, <400> field identifier
L:319 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
M:340 Repeated in SeqNo=14
L:346 M:283 W: Missing Blank Line separator, <400> field identifier
L:348 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
M:340 Repeated in SeqNo=15
L:375 M:283 W: Missing Blank Line separator, <400> field identifier
L:377 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16
M:340 Repeated in SeqNo=16
L:392 M:283 W: Missing Blank Line separator, <400> field identifier
L:394 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17
M:340 Repeated in SeqNo=17
L:409 M:283 W: Missing Blank Line separator, <400> field identifier
```

VERIFICATION SUMMARY   DATE: 06/07/2000
PATENT APPLICATION: US/09/521,640   TIME: 11:22:32

Input Set : D:\BACENDTAB_FINAL_RETREATS.rpt
Output Set: N:\CRF3\06072000\I521640.raw

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L:413 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
L:478 M:283 W: Missing Blank Line separator, <400> field identifier
L:480 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:22
M:340 Repeated in SeqNo=22
L:501 M:283 W: Missing Blank Line separator, <400> field identifier
L:503 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:23
M:340 Repeated in SeqNo=23
L:522 M:283 W: Missing Blank Line separator, <400> field identifier
L:526 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:24
L:535 M:283 W: Missing Blank Line separator, <400> field identifier
L:537 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:25
M:340 Repeated in SeqNo=25
L:576 M:283 W: Missing Blank Line separator, <400> field identifier
L:580 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:27
M:340 Repeated in SeqNo=27
L:595 M:283 W: Missing Blank Line separator, <400> field identifier
L:597 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
M:340 Repeated in SeqNo=28
L:618 M:283 W: Missing Blank Line separator, <400> field identifier
L:620 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:29
M:340 Repeated in SeqNo=29
L:649 M:283 W: Missing Blank Line separator, <400> field identifier
L:651 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:30
M:340 Repeated in SeqNo=30
L:668 M:283 W: Missing Blank Line separator, <400> field identifier
L:670 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:31
M:340 Repeated in SeqNo=31
L:687 M:283 W: Missing Blank Line separator, <400> field identifier
L:693 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:32
L:724 M:283 W: Missing Blank Line separator, <400> field identifier
L:726 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:34
M:340 Repeated in SeqNo=34
L:741 M:283 W: Missing Blank Line separator, <400> field identifier
L:758 M:283 W: Missing Blank Line separator, <400> field identifier
L:787 M:283 W: Missing Blank Line separator, <400> field identifier
L:810 M:283 W: Missing Blank Line separator, <400> field identifier
L:839 M:283 W: Missing Blank Line separator, <400> field identifier
L:860 M:283 W: Missing Blank Line separator, <400> field identifier
L:891 M:283 W: Missing Blank Line separator, <400> field identifier
L:908 M:283 W: Missing Blank Line separator, <400> field identifier
L:945 M:283 W: Missing Blank Line separator, <400> field identifier
L:964 M:283 W: Missing Blank Line separator, <400> field identifier
L:981 M:283 W: Missing Blank Line separator, <400> field identifier
L:1010 M:283 W: Missing Blank Line separator, <400> field identifier
L:1031 M:283 W: Missing Blank Line separator, <400> field identifier
L:1060 M:283 W: Missing Blank Line separator, <400> field identifier
L:1093 M:283 W: Missing Blank Line separator, <400> field identifier
L:1114 M:283 W: Missing Blank Line separator, <400> field identifier
L:1149 M:283 W: Missing Blank Line separator, <400> field identifier
```

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PATENT APPLICATION: US/09/521,640   TIME: 11:22:32

                Input Set : D:\BACENDTAB_FINAL_RETREATS.rpt
                Output Set: N:\CRF3\06072000\I521640.raw

L:1168 M:283 W: Missing Blank Line separator, <400> field identifier
L:1197 M:283 W: Missing Blank Line separator, <400> field identifier
L:1260 M:283 W: Missing Blank Line separator, <400> field identifier
L:1301 M:283 W: Missing Blank Line separator, <400> field identifier
L:1330 M:283 W: Missing Blank Line separator, <400> field identifier
L:1359 M:283 W: Missing Blank Line separator, <400> field identifier